fused to the VH chain, and thus all HuCAL VH chains in, and directly derived from, this vector have E (=GAA) at the first position (e.g. in pMx7_FS vector, see Figure 12).

Figure 12 Vector map and sequence (SEQ ID NO: 34) of scFv expression vector pMx7_FS_5D2. The expression vector pMx7_FS_5D2 leads to the expression of HuCAL scFv fragments (in Figure 12, the vector comprises a gene encoding a "dummy" antibody fragment called "5D2") when VH-CH1 is fused to a combination of a FLAG tag (Hopp et al., 1988; Knappik and Plückthun, 1994) and a STREP tag II (WSHPQFEK) (IBA GmbH, Göttingen, Germany; see: Schmidt and Skerra, 1993; Schmidt and Skerra, 1994; Schmidt et al., 1996; Voss and Skerra, 1997).

Figure 13 Vector map and sequence (SEQ ID NO: 35) of Fab expression vector pMx9_Fab_GPC8. The expression vector pMx9_Fab_GPC8 leads to the expression of HuCAL Fab fragments (in Figure 13, the vector comprises the Fab fragment MS-GPC8) when VH-CH1 is fused to a combination of a FLAG tag (Hopp et al., 1988; Knappik and Plückthun, 1994) and a STREP tag II (WSHPQFEK, SEQ ID No. 8) (IBA GmbH, Göttingen, Germany; see: Schmidt and Skerra, 1993; Schmidt and Skerra, 1994; Schmidt et al., 1996; Voss and Skerra, 1997). In pMx9_Fab vectors, the HuCAL Fab fragments cloned from the scFv fragments (see figure caption of Figure 11) do not have the short FLAG peptide sequence (DYKD, SEQ ID No. 9) fused to the VH chain, and all HuCAL VH chains in, and directly derived from, that vector have Q (=CAG) at the first position

Figure 14 Vector map and sequence (SEQ ID NO: 36) of Fab phage display vector pMORPH18_Fab_GPC8. The derivatives of vector pMORPH18 are phagemid vectors comprising a gene encoding a fusion between the C-terminal domain of the gene III protein of filamentous phage and the VH-CH1 chain of a HuCAL antibody. Additionally, the vector comprises the separately encoded VL-CL chain. In Figure 14, a vector comprising the Fab fragment MS-GPC-8 is shown. In pMORPH18_Fab vectors, the HuCAL Fab fragments cloned from the scFv fragments (see figure caption of Figure 11) do not have the short FLAG peptide sequence (DYKD, SEQ ID

No. 9) fused to the VH chain, and all HuCAL VH chains in, and directly derived from, that vector have Q (=CAG) at the first position.

Figure 15 Amino acid sequences of VH and VL domains of MS-GPC-1 (SEQ ID NOS 37-38, respectively), MS-GPC-6 (SEQ ID NOS 39-40, respectively), MS-GPC-8 (SEQ ID NOS 41-42, respectively), MS-GPC-10 (SEQ ID NOS 43-44, respectively), MS-GPC-8-6 (SEQ ID NOS 45-46, respectively), MS-GPC-8-10 (SEQ ID NOS 47-48, respectively), MS-GPC-8-17 (SEQ ID NOS 49-50, respectively), MS-GPC-8-27 (SEQ ID NOS 51-52, respectively), MS-GPC-8-6-13 (SEQ ID NOS 53-54, respectively), MS-GPC-8-10-57 (SEQ ID NOS 55-56, respectively), and MS-GPC-8-27-41 (SEQ ID NOS 57-58, respectively). The sequences in Figure 15 show amino acid 1 of VH as constructed in the original HuCAL master genes (Knappik et al. (2000): see Fig. 3 therein). In scFv constructs, as described in this application, amino acid 1 of VH is always E (see figure caption of Figure 11), in Fab constructs as described in this application, amino acid 1 of VH is always Q (see figure caption of Figure 13)

On Pages 77-79, in Tables 1 and 2, please enter the following text:

Table 1:

VH and VL families, VL CDR1 and VH/VL CDR 3 sequences of HLA-DR-specific polypeptides

Clone	VH	CDR3 Length	VH-CDR3-Seq.	VL	VL-CDR1-Seq.	CDR3 Length	VL-CDR3-Seq.	Families
MS-GPC-1	**H2**	**10**	**QYGHRGGFDH** (SEQ ID NO: 19)	**λ 1**	SGSSSNIGSNYVS (SEQ ID NO: 12)	**8**	**QSYDFNES** (SEQ ID NO: 63)	**H2 λ 1**
MS-GPC-6	**H3**	**9**	**GYGRYSPDL** (SEQ ID NO: 20)	**K3**	RASQSVSSSYLA (SEQ ID NO: 62)	**8**	**QQYSNLPF** (SEQ ID NO: 21)	**H3 K 3**
MS-GPC-8	**H2**	**10**	**SPRYRGAFDY** (SEQ ID NO: 3)	**λ 1**	SGSSSNIGSNYVS (SEQ ID NO: 12)	**8**	**QSYDMPQA** (SEQ ID NO: 22)	**H2 λ 1**
MS-GPC-10	**H2**	**10**	**QLHYRGGFDL** (SEQ ID NO: 61)	**λ 1**	SGSSSNIGSNYVS (SEQ ID NO: 12)	**8**	**QSYDLTMG** (SEQ ID NO: 23)	**H2 λ 1**
MS-GPC-8-1	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDFSHY** (SEQ ID NO: 24)	H2 λ 1
MS-GPC-8-6	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDYDHY** (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-9	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDIQLH** (SEQ ID NO: 25)	H2 λ 1
MS-GPC-8-10	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDLIRH** (SEQ ID NO: 4)	H2 λ 1
MS-GPC-8-17	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDFSVY** (SEQ ID NO: 26)	H2 λ 1
MS-GPC-8-18	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDFSIY** (SEQ ID NO: 27)	H2 λ 1
MS-GPC-8-27	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDMNVH** (SEQ ID NO: 5)	H2 λ 1
MS-GPC-8-6-2	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGSNYVH (SEQ ID NO: 13)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1

A 2 Cont.

MS-GPC-8-6-19	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGSNYVA (SEQ ID NO: 14)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-27	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSDSNIGANYVT (SEQ ID NO: 15)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-45	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSEPNIGSNYVF (SEQ ID NO: 28)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-13	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGANYVT (SEQ ID NO: 29)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-47	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGSNYVS (SEQ ID NO: 30)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-10-57	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGNNYVQ (SEQ ID NO: 7)	8	QSYDLIRH (SEQ ID NO: 4)	H2 λ 1
MS-GPC-8-27-7	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGNNYVG (SEQ ID NO: 31)	8	QSYDMNVH (SEQ ID NO: 5)	H2 λ 1
MS-GPC-8-27-10	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGANYVN (SEQ ID NO: 32)	8	QSYDMNVH (SEQ ID NO: 5)	H2 λ 1
MS-GPC-8-27-41	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGNNYVQ (SEQ ID NO: 7)	8	QSYDMNVH (SEQ ID NO: 5)	H2 λ 1

Table 2:

Steps in Antibody optimisation	Fab	k_{on} [$s^{-1}M^{-1}$] x 10^5 ± SD	k_{off} [s^{-1}] x 10^{-3} ± SD	K_D [nM] ± SD	L-CDR3	L-CDR1
Parental Fab	MS-GPC-8	0.99 ± 0.40	29.0 ± 8.40	346.1 ± 140.5[a)]	QSYDMPQA (SEQ ID NO: 59)	SGSSSNIGSNYVS (SEQ ID NO: 12)
L-CDR3-optim.	-8-1	1.93	20.9	108[e)]		
L-CDR3-optim.	-8-6	0.96 ± 0.14	5.48 ± 0.73	58.6 ± 11.7[b)]		
L-CDR3-optim.	-8-9	1.85	16.6	90.1 [e)]		
L-CDR3-optim.	-8-10	nd	7.0 [e)]	nd		
L-CDR3-optim.	-8-17	1.0	5.48	54.7 [e)]		
L-CDR3-optim.	-8-18	1.06	8.3	78.3 [e)]		
L-CDR3-optim.	-8-27	nd	6.6 [e)]	nd		
L-CDR3-optim.	-8-6	0.96 ± 0.14	5.48 ± 0.73	58.6 ± 11.7[b)]	QSYDYDHY (SEQ ID NO: 60)	SGSSSNIGSNYVS (SEQ ID NO: 12)
L-CDR3+1-opt.	-8-6-2	1.23 ± 0.11	0.94 ± 0.07	7.61 ± 0.25[c)]	QSYDYDHY (SEQ ID NO: 60)	SGSESNIGSNYVH (SEQ ID NO: 13)
L-CDR3+1-opt.	-8-6-19	1.10 ± 0.08	0.96 ± 0.15	8.74 ± 1.33[c)]	QSYDYDHY (SEQ ID NO: 60)	SGSESNIGSNYVA (SEQ ID NO: 14)
L-CDR3+1-opt.	-8-6-27	1.80 ± 0.24	1.10 ± 0.15	6.30 ± 0.63[d)]	QSYDYDHY (SEQ ID NO: 60)	SGSDSNIGANYVT (SEQ ID NO: 15)
L-CDR3+1-opt.	-8-6-45	1.20 ± 0.07	1.03 ± 0.04	8.63 ± 0.61[c)]	QSYDYDHY (SEQ ID NO: 60)	SGSEPNIGSNYVF (SEQ ID NO: 16)
L-CDR3+1-opt.	-8-6-13	1.90 ± 0.26	0.55 ± 0.05	2.96 ± 0.46[c)]	QSYDYDHY	SGSESNIGANYVT

					(SEQ ID NO: 60)	(SEQ ID NO: 15)
L-CDR3+1-opt.	-8-6-47	1.97 ± 0.29	0.62 ± 0.04	3.18 ± 0.33[c)]	QSYDYDHY (SEQ ID NO: 60)	SGSESNIGSNYVS (SEQ ID NO: 12)
L-CDR3+1-opt.	-8-10-57	1.65 ± 0.21	0.44 ± 0.06	2.67 ± 0.25[c)]	QSYDLIRH (SEQ ID NO: 4)	SGSESNIGNNYVQ (SEQ ID NO: 7)
L-CDR3+1-opt.	-8-27-7	1.74 ± 0.21	0.57 ± 0.07	3.30 ± 0.34[d)]	QSYDMNVH (SEQ ID NO: 5)	SGSESNIGNNYVG (SEQ ID NO: 17)
L-CDR3+1-opt.	-8-27-10	1.76 ± 0.21	0.53 ± 0.05	3.01 ± 0.21[c)]	QSYDMNVH (SEQ ID NO: 5)	SGSESNIGANYVN (SEQ ID NO: 18)
L-CDR3+1-opt.	-8-27-41	1.67 ± 0.16	0.49 ± 0.03	2.93 ± 0.27[d)]	QSYDMNVH (SEQ ID NO: 5)	SGSESNIGNNYVQ (SEQ ID NO: 7)

a) Affinity data of MS-GPC-8 are based on 8 different Fab-preparations which were measured on 4 different chips (2 x 500, 1000, 4000RU)
b) For MS-GPC-8-6 mean and standard deviation of 3 different preparations on 3 different chips (500, 4000, 3000RU) is shown.
c) 3000RU MHCII were immobilized on a CM5-chip. For each measurement 7 different concentrations from 1µM to 16nM were injected on the surface. Dissociation time: 150sec, regeneration was reached by 6µl 10mM Glycine pH2.3 followed by 8µl 7.5mM NaOH. For MS-GPC-8-6-19 mean and standard deviation of 4 different preparations are shown whereas for all other binders mean and standard deviation of 3 different preparations are shown.
d) One protein preparation is measured on 3 different chips (3000, 2800 and 6500RU).
e) Affinity determination of maturated MHCII binder on a 4000RU density chips; single measurement.
Molecular weights were determined after size exclusion chromatography and found 100% monomeric with the right molecular weight between 45 and 48 kDa.

The replacement paragraphs presented above incorporate changes as indicated by the marked-up versions below.

Figure 11 Vector map and sequence (SEQ ID NO: 33) of scFv phage display vector pMORPH13_scFv. The vector pMORPH13_scFv is a phagemid vector comprising a gene encoding a fusion between the C-terminal domain of the gene III protein of filamentous phage and a HuCAL scFv. In Figure 11, a vector comprising a model scFv gene (combination of VH1A and Vλ3 (Knappik et al., 2000) is shown. The original HuCAL master genes (Knappik et al. (2000): see Fig. 3 therein) have been constructed with their authentic N-termini: VH1A, VH1B, VH2, VH4 and VH6 with Q (=CAG) as the first amino acid. VH3 and VH5 with E (=GAA) as the first amino acid. Vector pMORPH13_scFv comprises the short FLAG peptide sequence (DYKD) fused to the VH chain, and thus all HuCAL VH chains in, and directly derived from, this vector have E (=GAA) at the first position (e.g. in pMx7_FS vector, see Figure 12).

Figure 12 Vector map and sequence (SEQ ID NO: 34) of scFv expression vector pMx7_FS_5D2. The expression vector pMx7_FS_5D2 leads to the expression of HuCAL scFv fragments (in Figure 12, the vector comprises a gene encoding a "dummy" antibody fragment called "5D2") when VH-CH1 is fused to a combination of a FLAG tag (Hopp et al., 1988; Knappik and Plückthun, 1994) and a STREP tag II (WSHPQFEK) (IBA GmbH, Göttingen, Germany; see: Schmidt and Skerra, 1993; Schmidt and Skerra, 1994; Schmidt et al., 1996; Voss and Skerra, 1997).

Figure 13 Vector map and sequence (SEQ ID NO: 35) of Fab expression vector pMx9_Fab_GPC8. The expression vector pMx9_Fab_GPC8 leads to the expression of HuCAL Fab fragments (in Figure 13, the vector comprises the Fab fragment MS-GPC8) when VH-CH1 is fused to a combination of a FLAG tag (Hopp et al., 1988; Knappik and Plückthun, 1994) and a STREP tag II (WSHPQFEK, SEQ ID No. 8) (IBA GmbH, Göttingen, Germany; see: Schmidt and Skerra, 1993; Schmidt and Skerra, 1994; Schmidt et al., 1996; Voss and Skerra, 1997). In pMx9_Fab vectors, the

HuCAL Fab fragments cloned from the scFv fragments (see figure caption of Figure 11) do not have the short FLAG peptide sequence (DYKD, SEQ ID No. 9) fused to the VH chain, and all HuCAL VH chains in, and directly derived from, that vector have Q (=CAG) at the first position

Figure 14 Vector map and sequence (SEQ ID NO: 36) of Fab phage display vector pMORPH18_Fab_GPC8. The derivatives of vector pMORPH18 are phagemid vectors comprising a gene encoding a fusion between the C-terminal domain of the gene III protein of filamentous phage and the VH-CH1 chain of a HuCAL antibody. Additionally, the vector comprises the separately encoded VL-CL chain. In Figure 14, a vector comprising the Fab fragment MS-GPC-8 is shown. In pMORPH18_Fab vectors, the HuCAL Fab fragments cloned from the scFv fragments (see figure caption of Figure 11) do not have the short FLAG peptide sequence (DYKD, SEQ ID No. 9) fused to the VH chain, and all HuCAL VH chains in, and directly derived from, that vector have Q (=CAG) at the first position.

Figure 15 Amino acid sequences of VH and VL domains of MS-GPC-1 (SEQ ID NOS 37-38, respectively), MS-GPC-6 (SEQ ID NOS 39-40, respectively), MS-GPC-8 (SEQ ID NOS 41-42, respectively), MS-GPC-10 (SEQ ID NOS 43-44, respectively), MS-GPC-8-6 (SEQ ID NOS 45-46, respectively), MS-GPC-8-10 (SEQ ID NOS 47-48, respectively), MS-GPC-8-17 (SEQ ID NOS 49-50, respectively), MS-GPC-8-27 (SEQ ID NOS 51-52, respectively), MS-GPC-8-6-13 (SEQ ID NOS 53-54, respectively), MS-GPC-8-10-57 (SEQ ID NOS 55-56, respectively), and MS-GPC-8-27-41 (SEQ ID NOS 57-58, respectively). The sequences in Figure 15 show amino acid 1 of VH as constructed in the original HuCAL master genes (Knappik et al. (2000): see Fig. 3 therein). In scFv constructs, as described in this application, amino acid 1 of VH is always E (see figure caption of Figure 11), in Fab constructs as described in this application, amino acid 1 of VH is always Q (see figure caption of Figure 13)

Table 1:

VH and VL families, VL CDR1 and VH/VL CDR 3 sequences of HLA-DR-specific polypeptides

Clone	VH	CDR3 Length	VH-CDR3-Seq.	VL	VL-CDR1-Seq.	CDR3 Length	VL-CDR3-Seq.	Families
MS-GPC-1	**H2**	**10**	**QYGHRGGFDH** (SEQ ID NO: 19)	**λ 1**	SGSSSNIGSNYVS (SEQ ID NO: 12)	**8**	**QSYDFNES** (SEQ ID NO: 63)	**H2 λ 1**
MS-GPC-6	**H3**	**9**	**GYGRYSPDL** (SEQ ID NO: 20)	**K3**	RASQSVSSSYLA (SEQ ID NO: 62)	**8**	**QQYSNLPF** (SEQ ID NO: 21)	**H3 K 3**
MS-GPC-8	**H2**	**10**	**SPRYRGAFDY** (SEQ ID NO: 3)	**λ 1**	SGSSSNIGSNYVS (SEQ ID NO: 12)	**8**	**QSYDMPQA** (SEQ ID NO: 22)	**H2 λ 1**
MS-GPC-10	**H2**	**10**	**QLHYRGGFDL** (SEQ ID NO: 61)	**λ 1**	SGSSSNIGSNYVS (SEQ ID NO: 12)	**8**	**QSYDLTMG** (SEQ ID NO: 23)	**H2 λ 1**
MS-GPC-8-1	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDFSHY** (SEQ ID NO: 24)	H2 λ 1
MS-GPC-8-6	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDYDHY** (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-9	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDIQLH** (SEQ ID NO: 25)	H2 λ 1
MS-GPC-8-10	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDLIRH** (SEQ ID NO: 4)	H2 λ 1
MS-GPC-8-17	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDFSVY** (SEQ ID NO: 26)	H2 λ 1
MS-GPC-8-18	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDFSIY** (SEQ ID NO: 27)	H2 λ 1
MS-GPC-8-27	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSSSNIGSNYVS (SEQ ID NO: 12)	8	**QSYDMNVH** (SEQ ID NO: 5)	H2 λ 1
MS-GPC-8-6-2	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGSNYVH (SEQ ID NO: 13)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1

MS-GPC-8-6-19	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGSNYVA (SEQ ID NO: 14)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-27	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSDSNIGANYVT (SEQ ID NO: 15)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-45	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSEPNIGSNYVF (SEQ ID NO: 28)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-13	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGANYVT (SEQ ID NO: 29)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-6-47	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGSNYVS (SEQ ID NO: 30)	8	QSYDYDHY (SEQ ID NO: 60)	H2 λ 1
MS-GPC-8-10-57	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGNNYVQ (SEQ ID NO: 7)	8	QSYDLIRH (SEQ ID NO: 4)	H2 λ 1
MS-GPC-8-27-7	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGNNYVG (SEQ ID NO: 31)	8	QSYDMNVH (SEQ ID NO: 5)	H2 λ 1
MS-GPC-8-27-10	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGANYVN (SEQ ID NO: 32)	8	QSYDMNVH (SEQ ID NO: 5)	H2 λ 1
MS-GPC-8-27-41	H2	10	SPRYRGAFDY (SEQ ID NO: 3)	λ 1	SGSESNIGNNYVQ (SEQ ID NO: 7)	8	QSYDMNVH (SEQ ID NO: 5)	H2 λ 1

Table 2:

Steps in Antibody optimisation	Fab	k_{on} [$s^{-1}M^{-1}$] x 10^5 ± SD	k_{off} [s^{-1}] x 10^{-3} ± SD	K_D [nM] ± SD	L-CDR3	L-CDR1
Parental Fab	MS-GPC-8	0.99 ± 0.40	29.0 ± 8.40	346.1 ± 140.5[a)]	QSYDMPQA (SEQ ID NO: 59)	SGSSSNIGSNYVS (SEQ ID NO: 12)
L-CDR3-optim.	-8-1	1.93	20.9	108[e)]		
L-CDR3-optim.	-8-6	0.96 ± 0.14	5.48 ± 0.73	58.6 ± 11.7[b)]		
L-CDR3-optim.	-8-9	1.85	16.6	90.1 [e)]		
L-CDR3-optim.	-8-10	nd	7.0 [e)]	nd		
L-CDR3-optim.	-8-17	1.0	5.48	54.7 [e)]		
L-CDR3-optim.	-8-18	1.06	8.3	78.3 [e)]		
L-CDR3-optim.	-8-27	nd	6.6 [e)]	nd		
L-CDR3-optim.	-8-6	0.96 ± 0.14	5.48 ± 0.73	58.6 ± 11.7[b)]	QSYDYDHY (SEQ ID NO: 60)	SGSSSNIGSNYVS (SEQ ID NO: 12)
L-CDR3+1-opt.	-8-6-2	1.23 ± 0.11	0.94 ± 0.07	7.61 ± 0.25[c)]	QSYDYDHY (SEQ ID NO: 60)	SGSESNIGSNYVH (SEQ ID NO: 13)
L-CDR3+1-opt.	-8-6-19	1.10 ± 0.08	0.96 ± 0.15	8.74 ± 1.33[c)]	QSYDYDHY (SEQ ID NO: 60)	SGSESNIGSNYVA (SEQ ID NO: 14)
L-CDR3+1-opt.	-8-6-27	1.80 ± 0.24	1.10 ± 0.15	6.30 ± 0.63[d)]	QSYDYDHY (SEQ ID NO: 60)	SGSDSNIGANYVT (SEQ ID NO: 15)
L-CDR3+1-opt.	-8-6-45	1.20 ± 0.07	1.03 ± 0.04	8.63 ± 0.61[c)]	QSYDYDHY (SEQ ID NO: 60)	SGSEPNIGSNYVF (SEQ ID NO: 16)
L-CDR3+1-opt.	-8-6-13	1.90 ± 0.26	0.55 ± 0.05	2.96 ± 0.46[c)]	QSYDYDHY	SGSESNIGANYVT

					(SEQ ID NO: 60)	(SEQ ID NO: 15)
L-CDR3+1-opt.	-8-6-47	1.97 ± 0.29	0.62 ± 0.04	3.18 ± 0.33[c)]	QSYDYDHY (SEQ ID NO: 60)	SGSESNIGSNYVS (SEQ ID NO: 12)
L-CDR3+1-opt.	-8-10-57	1.65 ± 0.21	0.44 ± 0.06	2.67 ± 0.25[c)]	QSYDLIRH (SEQ ID NO: 4)	SGSESNIGNNYVQ (SEQ ID NO: 7)
L-CDR3+1-opt.	-8-27-7	1.74 ± 0.21	0.57 ± 0.07	3.30 ± 0.34[d)]	QSYDMNVH (SEQ ID NO: 5)	SGSESNIGNNYVG (SEQ ID NO: 17)
L-CDR3+1-opt.	-8-27-10	1.76 ± 0.21	0.53 ± 0.05	3.01 ± 0.21[c)]	QSYDMNVH (SEQ ID NO: 5)	SGSESNIGANYVN (SEQ ID NO: 18)
L-CDR3+1-opt.	-8-27-41	1.67 ± 0.16	0.49 ± 0.03	2.93 ± 0.27[d)]	QSYDMNVH (SEQ ID NO: 5)	SGSESNIGNNYVQ (SEQ ID NO: 7)

a) Affinity data of MS-GPC-8 are based on 8 different Fab-preparations which were measured on 4 different chips (2 x 500, 1000, 4000RU)
b) For MS-GPC-8-6 mean and standard deviation of 3 different preparations on 3 different chips (500, 4000, 3000RU) is shown.
c) 3000RU MHCII were immobilized on a CM5-chip. For each measurement 7 different concentrations from 1µM to 16nM were injected on the surface. Dissociation time: 150sec, regeneration was reached by 6µl 10mM Glycine pH2.3 followed by 8µl 7.5mM NaOH. For MS-GPC-8-6-19 mean and standard deviation of 4 different preparations are shown whereas for all other binders mean and standard deviation of 3 different preparations are shown.
d) One protein preparation is measured on 3 different chips (3000, 2800 and 6500RU).
e) Affinity determination of maturated MHCII binder on a 4000RU density chips; single measurement.
Molecular weights were determined after size exclusion chromatography and found 100% monomeric with the right molecular weight between 45 and 48 kDa.

If there are any fees due in connection with the filing of this Preliminary Amendment, please charge the fees to our **Deposit Account No. 18-1945.** Please direct any questions arising from this submission to the undersigned at (617) 951-7085.

Respectfully Submitted,

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David P. Halstead
Registration No. 44,735

Customer No: 28120
Docketing Specialist
Ropes & Gray
One International Place
Boston, MA 02110
Phone: 617-951-7615
Fax: 617-951-7050